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1652

PCT09

#8/8/02

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/869,446

DATE: 07/12/2001

TIME: 07:46:28

Input Set : A:\sequence.listing.txt

Output Set: N:\CRF3\07122001\I869446.raw

5 <110> APPLICANT: UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC.
6 Przybyla, Alan
7 Menon, Nanda
10 <120> TITLE OF INVENTION: RUBREDOXIN FUSION PROTEINS, PROTEIN EXPRESSION SYSTEM
11 AND METHODS
13 <130> FILE REFERENCE: 235.00040201
C--> 16 <140> CURRENT APPLICATION NUMBER: US/09/869,446
C--> 17 <141> CURRENT FILING DATE: 2001-06-27
20 <150> PRIOR APPLICATION NUMBER: 60/114,034
21 <151> PRIOR FILING DATE: 1998-12-29
24 <160> NUMBER OF SEQ ID NOS: 14
27 <170> SOFTWARE: PatentIn Ver. 2.0
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 276
32 <212> TYPE: DNA
33 <213> ORGANISM: Artificial Sequence
35 <220> FEATURE:
36 <223> OTHER INFORMATION: Description of Artificial Sequence: portion of
37 prUBEX
39 <400> SEQUENCE: 1
40 catatgaaaa agtacgtatg caccgtctgc ggttacgaat acgaccctgc tgaaggcgac 60
41 cccgacaacg gcggtgaagcc cggcacctcg ttcgacgacc tgccggccga ctgggtatgc 120
42 cccgtgtgcg gcgcccccaa gagcgaattc gaagccgcca tgcattggcg atccgaattc 180
43 gagaaccatc atcatcatca tcacaacgac tacaaggacg acgatgacaa ggatctgcag 240
44 agatcttcgg gtacccgcaa gcttgccggc gcaactc 276
46 <210> SEQ ID NO: 2
47 <211> LENGTH: 76
48 <212> TYPE: PRT
49 <213> ORGANISM: Artificial Sequence
51 <220> FEATURE:
52 <223> OTHER INFORMATION: Description of Artificial Sequence: modified
53 rubredoxin including affinity tag, flag peptide
54 and enterokinase site
56 <400> SEQUENCE: 2
57 Met Lys Lys Tyr Val Cys Thr Val Cys Gly Tyr Glu Tyr Asp Pro Ala
58 1 5 10 15
59 Glu Gly Asp Pro Asp Asn Gly Val Lys Pro Gly Thr Ser Phe Asp Asp
60 20 25 30
61 Leu Pro Ala Asp Trp Val Cys Pro Val Cys Gly Ala Pro Lys Ser Glu
62 35 40 45
63 Phe Glu Ala Ala Met His Gly Gly Ser Glu Phe Glu Asn His His His
64 50 55 60
65 His His His Asn Asp Tyr Lys Asp Asp Asp Asp Lys
66 65 70 75
69 <210> SEQ ID NO: 3
70 <211> LENGTH: 52
71 <212> TYPE: PRT

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72 <213> ORGANISM: Desulfovibrio vulgaris
74 <400> SEQUENCE: 3
75 Met Lys Lys Tyr Val Cys Thr Val Cys Gly Tyr Glu Tyr Asp Pro Ala
76   1           5           10           15
77 Glu Gly Asp Pro Asp Asn Gly Val Lys Pro Gly Thr Ser Phe Asp Asp
78           20           25           30
79 Leu Pro Ala Asp Trp Val Cys Pro Val Cys Gly Ala Pro Lys Ser Glu
80           35           40           45
81 Phe Glu Ala Ala
82   50
85 <210> SEQ ID NO: 4
86 <211> LENGTH: 6
87 <212> TYPE: PRT
88 <213> ORGANISM: Artificial Sequence
90 <220> FEATURE:
91 <223> OTHER INFORMATION: Description of Artificial Sequence: affinity tag
93 <400> SEQUENCE: 4
94 His His His His His His
95   1           5
98 <210> SEQ ID NO: 5
99 <211> LENGTH: 8
100 <212> TYPE: PRT
101 <213> ORGANISM: Artificial Sequence
103 <220> FEATURE:
104 <223> OTHER INFORMATION: Description of Artificial Sequence: Flag peptide
106 <400> SEQUENCE: 5
107 Asp Tyr Lys Asp Asp Asp Asp Lys
108   1           5
111 <210> SEQ ID NO: 6
112 <211> LENGTH: 5
113 <212> TYPE: PRT
114 <213> ORGANISM: Artificial Sequence
116 <220> FEATURE:
117 <223> OTHER INFORMATION: Description of Artificial Sequence: enterokinase
118   site
121 <400> SEQUENCE: 6
122 Asp Asp Asp Asp Lys
123   1           5
126 <210> SEQ ID NO: 7
127 <211> LENGTH: 4
128 <212> TYPE: PRT
129 <213> ORGANISM: Artificial Sequence
131 <220> FEATURE:
132 <223> OTHER INFORMATION: Description of Artificial Sequence: affinity tag
135 <400> SEQUENCE: 7
136 His Gly Leu His
137   1
140 <210> SEQ ID NO: 8
141 <211> LENGTH: 381

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142 <212> TYPE: DNA
143 <213> ORGANISM: Artificial Sequence
145 <220> FEATURE:
146 <223> OTHER INFORMATION: Description of Artificial Sequence: A 1-42
147     rubredoxin fusion construct
150 <400> SEQUENCE: 8
151 atgaaaaagt acgtatgcac cgtctgcggt tacgaatacg accctgctga aggcgacccc 60
152 gacaacggcg tgaagcccg cacctcggtc gacgacctgc cggccgactt gggtagccc 120
153 cgtgtgcggc gcccccaaga gcgaattcga agccgccatg catggcggat ccgaattcga 180
154 gaaccatcat catcatcatc acaacgacta caaggacgac gatgacgacg atgacaagga 240
155 tctgatcgaa ggtcgtgatg cagaattccg acaatgactca ggatatgaag ttcatcatca 300
156 aaaattggtg ttctttgcag aagatgtggg ttcaaacaaa ggtgcaatca ttggactcat 360
157 ggtgggcggt gttgtcatag c                                     381
160 <210> SEQ ID NO: 9
161 <211> LENGTH: 124
162 <212> TYPE: PRT
163 <213> ORGANISM: Artificial Sequence
165 <220> FEATURE:
166 <223> OTHER INFORMATION: Description of Artificial Sequence: A 1-42
167     rubredoxin fusion protein
170 <400> SEQUENCE: 9
171 Met Lys Lys Tyr Val Cys Thr Val Cys Gly Tyr Glu Tyr Asp Pro Ala
172   1           5           10           15
173 Glu Gly Asp Pro Asp Asn Gly Val Lys Pro Gly Thr Ser Phe Asp Asp
174           20           25           30
175 Leu Pro Ala Asp Trp Val Cys Pro Val Cys Gly Ala Pro Lys Ser Glu
176           35           40           45
177 Phe Glu Ala Ala Met His Gly Gly Ser Glu Phe Glu Asn His His His
178           50           55           60
179 His His His Asn Asp Tyr Lys Asp Asp Asp Asp Lys Asp Leu Ile Glu
180           65           70           75           80
181 Gly Arg Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His
182           85           90           95
183 Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala
184           100          105          110
185 Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala
186           115          120
189 <210> SEQ ID NO: 10
190 <211> LENGTH: 42
191 <212> TYPE: PRT
192 <213> ORGANISM: Artificial Sequence
194 <220> FEATURE:
195 <223> OTHER INFORMATION: Description of Artificial Sequence: A 1-42
196     peptide
198 <400> SEQUENCE: 10
199 Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys
200   1           5           10           15
201 Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile
202           20           25           30

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203 Gly Leu Met Val Gly Gly Val Val Ile Ala
204           35           40
208 <210> SEQ ID NO: 11
209 <211> LENGTH: 4
210 <212> TYPE: PRT
211 <213> ORGANISM: Artificial Sequence
213 <220> FEATURE:
214 <223> OTHER INFORMATION: Description of Artificial Sequence: Factor Xa
215     restriction site
218 <400> SEQUENCE: 11
219 Ile Glu Gly Arg
220   1
223 <210> SEQ ID NO: 12
224 <211> LENGTH: 30
225 <212> TYPE: PRT
226 <213> ORGANISM: Artificial Sequence
228 <220> FEATURE:
229 <223> OTHER INFORMATION: Description of Artificial Sequence: intervening
230     spacer region
232 <400> SEQUENCE: 12
233 Met His Gly Gly Ser Glu Phe Glu Asn His His His His His Asn
234   1           5           10           15
235 Asp Tyr Lys Asp Asp Asp Asp Lys Asp Leu Ile Glu Gly Arg
236           20           25           30
241 <210> SEQ ID NO: 13
242 <211> LENGTH: 7
243 <212> TYPE: PRT
244 <213> ORGANISM: Artificial Sequence
246 <220> FEATURE:
247 <223> OTHER INFORMATION: Description of Artificial Sequence: Flag peptide
250 <400> SEQUENCE: 13
251 Tyr Lys Asp Asp Asp Asp Lys
252   1           5
255 <210> SEQ ID NO: 14
256 <211> LENGTH: 40
257 <212> TYPE: PRT
258 <213> ORGANISM: Artificial Sequence
260 <220> FEATURE:
261 <223> OTHER INFORMATION: Description of Artificial Sequence: A 1-40
262     peptide
265 <400> SEQUENCE: 14
266 Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys
267   1           5           10           15
268 Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile
269           20           25           30
270 Gly Leu Met Val Gly Gly Val Val
271           35           40

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VERIFICATION SUMMARY

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L:16 M:270 C: Current Application Number differs, Replaced Current Application Number

L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date